

[illegible]

CCTGTGGGAG AGAGCGCCGG GATCCGGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT 60  
 GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACA CGAGCGCCTC GGCCTAACC 120

9

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-2-

GAGTGTTCGC	GGGGGCTGTG	AGGGGAGGGC	CCCGGGCGCC	ATTGCTGGCG	GTGGGAGCGC	180
CGCCCCGTCT	CAGCCCCCCC	TCGGCTGCTC	TCCTCCTCCG	GCTGGGAGGG	GCCGTATCTC	240
GGGGCCGTCG	CCAGCCCCCG	CCCGGGCTCG	ATAATCAAGG	GCCTCGGCCG	TCGTCCCCGA	300
CCTCATTCCA	TCGCCCTTGC	CGGGCAGCCC	GGGCAGAGAC	C ATG TTT GAC AAG		353
				Met Phe Asp Lys		
				1		
ACG CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT						401
Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala						
5			10		15	20
GGA TTG CCT TTT GCA ATT CTT ACT TCA AGG CAT ACC CCC TTC CAA CGA						449
Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr Pro Phe Gln Arg						
		25		30		35
GGA GTA TTC TGT AAT GAT GAG TCC ATC AAG TAC CCT TAC AAA GAA GAC						497
Gly Val Phe Cys Asn Asp Glu Ser Ile Lys Tyr Pro Tyr Lys Glu Asp						
		40		45		50
ACC ATA CCT TAT GCG TTA TTA GGT GGA ATA ATC ATT CCA TTC AGT ATT						545
Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Ile Ile Pro Phe Ser Ile						
		55		60		65
ATC GTT ATT ATT CTT GGA GAA ACC CTG TCT GTT TAC TGT AAC CTT TTG						593
Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr Cys Asn Leu Leu						
		70		75		80
CAC TCA AAT TCC TTT ATC AGG AAT AAC TAC ATA GCC ACT ATT TAC AAA						641
His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala Thr Ile Tyr Lys						
		85		90		100
GCC ATT GGA ACC TTT TTA TTT GGT GCA GCT GCT AGT CAG TCC CTG ACT						689
Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser Gln Ser Leu Thr						
			105		110	115
GAC ATT GCC AAG TAT TCA ATA GGC AGA CTG CGG CCT CAC TTC TTG GAT						737
Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro His Phe Leu Asp						
			120		125	130
GTT TGT GAT CCA GAT TGG TCA AAA ATC AAC TGC AGC GAT GGT TAC ATT						785
Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser Asp Gly Tyr Ile						
		135			140	145
GAA TAC TAC ATA TGT CGA GGG AAT GCA GAA AGA GTT AAG GAA GGC AGG						833
Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val Lys Glu Gly Arg						
		150			155	160
TTG TCC TTC TAT TCA GGC CAC TCT TCG TTT TCC ATG TAC TGC ATG CTG						881
Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met Tyr Cys Met Leu						
		165		170		175
TTT GTG GCA CTT TAT CTT CAA GCC AGG ATG AAG GGA GAC TGG GCA AGA						929
Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly Asp Trp Ala Arg						
			185		190	195
CTC TTA CGC CCC ACA CTG CAA TTT GGT CTT GTT GCC GTA TCC ATT TAT						977
Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala Val Ser Ile Tyr						
		200			205	210
GTG GGC CTT TCT CGA GTT TCT GAT TAT AAA CAC CAC TGG AGC GAT GTG						1025
Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His Trp Ser Asp Val						
		215			220	225

000400 200400 400400

(2) INFORMATION FOR SEQ ID NO:2:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met 1	Phe	Asp	Lys	Thr 5	Arg	Leu	Pro	Tyr	Val 10	Ala	Leu	Asp	Val	Leu 15	Cys
Val	Leu	Leu	Ala 20	Gly	Leu	Pro	Phe	Ala 25	Ile	Leu	Thr	Ser	Arg 30	His	Thr
Pro	Phe	Gln 35	Arg	Gly	Val	Phe	Cys 40	Asn	Asp	Glu	Ser	Ile 45	Lys	Tyr	Pro
Tyr	Lys 50	Glu	Asp	Thr	Ile	Pro 55	Tyr	Ala	Leu	Leu	Gly 60	Gly	Ile	Ile	Ile
Pro 65	Phe	Ser	Ile	Ile	Val 70	Ile	Ile	Leu	Gly	Glu 75	Thr	Leu	Ser	Val	Tyr 80
Cys	Asn	Leu	Leu	His 85	Ser	Asn	Ser	Phe	Ile 90	Arg	Asn	Asn	Tyr	Ile 95	Ala
Thr	Ile	Tyr	Lys 100	Ala	Ile	Gly	Thr	Phe 105	Leu	Phe	Gly	Ala	Ala 110	Ala	Ser
Gln	Ser	Leu 115	Thr	Asp	Ile	Ala	Lys 120	Tyr	Ser	Ile	Gly	Arg 125	Leu	Arg	Pro
His	Phe 130	Leu	Asp	Val	Cys	Asp 135	Pro	Asp	Trp	Ser	Lys 140	Ile	Asn	Cys	Ser

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Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val  
145 150 155 160

Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met  
165 170 175

Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly  
180 185 190

Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala  
195 200 205

Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His  
210 215 220

Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile  
225 230 235 240

Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe  
245 250 255

Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro  
260 265 270

Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro  
275 280

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1566 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 342..1196

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 342..1196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTGTGGGAG AGAGCGCCGG GATCCGACG GGGTAGCAAC CGGGGCAGGC CGTGCCGGCT	60
GAGGAGGTCC TGAGGCTACA GAGCTGCCGC GGCTGGCACA CGAGCGCCTC GGCCTAACC	120
GAGTGTTCGC GGGGGCTGTG AGGGGAGGGC CCCGGGCGCC ATTGCTGGCG GTGGGAGCGC	180
CGCCCGGTCT CAGCCCGCCC TCGGCTGCTC TCCTCCTCCG GCTGGGAGGG GCCGTATCTC	240
GGGGCCGTCG CCAGCCCCGG CCCGGGCTCG ATAATCAAGG GCCTCGGCCG TCGTCCCGCA	300
CCTCATTCCA TCGCCCTTGC CGGGCAGCCC GGGCAGAGAC C ATG TTT GAC AAG	353
Met Phe Asp Lys	
1	
ACG CGG CTG CCG TAC GTG GCC CTC GAT GTG CTC TGC GTG TTG CTG GCT	401
Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys Val Leu Leu Ala	
5 10 15 20	

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TCC	ATG	CCT	ATG	GCT	GTT	CTA	AAA	TTG	GGC	CAA	ATA	TAT	CCA	TTT	CAG	449
Ser	Met	Pro	Met	Ala	Val	Leu	Lys	Leu	Gly	Gln	Ile	Tyr	Pro	Phe	Gln	
				25					30					35		
AGA	GGC	TTT	TTC	TGT	AAA	GAC	AAC	AGC	ATC	AAC	TAT	CCG	TAC	CAT	GAC	497
Arg	Gly	Phe	Phe	Cys	Lys	Asp	Asn	Ser	Ile	Asn	Tyr	Pro	Tyr	His	Asp	
			40					45					50			
AGT	ACC	GCC	GCA	TCC	ACT	GTC	CTC	ATC	CTA	GTG	GGG	GTT	GGC	TTG	CCC	545
Ser	Thr	Ala	Ala	Ser	Thr	Val	Leu	Ile	Leu	Val	Gly	Val	Gly	Leu	Pro	
		55					60					65				
GTT	TCC	TCT	ATT	ATT	CTT	GGA	GAA	ACC	CTG	TCT	GTT	TAC	TGT	AAC	CTT	593
Val	Ser	Ser	Ile	Ile	Leu	Gly	Glu	Thr	Leu	Ser	Val	Tyr	Cys	Asn	Leu	
	70					75					80					
TTG	CAC	TCA	AAT	TCC	TTT	ATC	AGT	AAT	AAC	TAC	ATA	GCC	ACT	ATT	TAC	641
Leu	His	Ser	Asn	Ser	Phe	Ile	Ser	Asn	Asn	Tyr	Ile	Ala	Thr	Ile	Tyr	
	85				90					95					100	
AAA	GCC	ATT	GGA	ACC	TTT	TTA	TTT	GGT	GCA	GCT	GCT	AGT	CAG	TCC	CTG	689
Lys	Ala	Ile	Gly	Thr	Phe	Leu	Phe	Gly	Ala	Ala	Ala	Ser	Gln	Ser	Leu	
				105					110					115		
ACT	GAC	ATT	GCC	AAG	TAT	TCA	ATA	GGC	AGA	CTG	CGG	CCT	CAC	TTC	TTG	737
Thr	Asp	Ile	Ala	Lys	Tyr	Ser	Ile	Gly	Arg	Leu	Arg	Pro	His	Phe	Leu	
			120					125					130			
GAT	GTT	TGT	GAT	CCA	GAT	TGG	TCA	AAA	ATC	AAC	TGC	AGC	GAT	GGT	TAC	785
Asp	Val	Cys	Asp	Pro	Asp	Trp	Ser	Lys	Ile	Asn	Cys	Ser	Asp	Gly	Tyr	
		135				140						145				
ATT	GAA	TAC	TAC	ATA	TGT	CGA	GGG	AAT	GCA	GAA	AGA	GTT	AAG	GAA	GGC	833
Ile	Glu	Tyr	Tyr	Ile	Cys	Arg	Gly	Asn	Ala	Glu	Arg	Val	Lys	Glu	Gly	
	150					155					160					
AGG	TTG	TCC	TTC	TAT	TCA	GGC	CAC	TCT	TCG	TTT	TCC	ATG	TAC	TGC	ATG	881
Arg	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	Phe	Ser	Met	Tyr	Cys	Met	
	165				170					175					180	
CTG	TTT	GTG	GCA	CTT	TAT	CTT	CAA	GCC	AGG	ATG	AAG	GGA	GAC	TGG	GCA	929
Leu	Phe	Val	Ala	Leu	Tyr	Leu	Gln	Ala	Arg	Met	Lys	Gly	Asp	Trp	Ala	
				185					190					195		
AGA	CTC	TTA	CGC	CCC	ACA	CTG	CAA	TTT	GGT	CTT	GTT	GCC	GTA	TCC	ATT	977
Arg	Leu	Leu	Arg	Pro	Thr	Leu	Gln	Phe	Gly	Leu	Val	Ala	Val	Ser	Ile	
			200					205					210			
TAT	GTG	GGC	CTT	TCT	CGA	GTT	TCT	GAT	TAT	AAA	CAC	CAC	TGG	AGC	GAT	1025
Tyr	Val	Gly	Leu	Ser	Arg	Val	Ser	Asp	Tyr	Lys	His	His	Trp	Ser	Asp	
		215					220					225				
GTG	TTG	ACT	GGA	CTC	ATT	CAG	GGA	GCT	CTG	GTT	GCA	ATA	TTA	GTT	GCT	1073
Val	Leu	Thr	Gly	Leu	Ile	Gln	Gly	Ala	Leu	Val	Ala	Ile	Leu	Val	Ala	
	230					235					240					
GTA	TAT	GTA	TCG	GAT	TTC	TTC	AAA	GAA	AGA	ACT	TCT	TTT	AAA	GAA	AGA	1121
Val	Tyr	Val	Ser	Asp	Phe	Phe	Lys	Glu	Arg	Thr	Ser	Phe	Lys	Glu	Arg	
	245				250					255				260		
AAA	GAG	GAG	GAC	TCT	CAT	ACA	ACT	CTG	CAT	GAA	ACA	CCA	ACA	ACT	GGG	1169
Lys	Glu	Glu	Asp	Ser	His	Thr	Thr	Leu	His	Glu	Thr	Pro	Thr	Thr	Gly	
				265					270					275		
AAT	CAC	TAT	CCG	AGC	AAT	CAC	CAG	CCT	TGAAAGGCAG	CAGGGTGCCC						1216
Asn	His	Tyr	Pro	Ser	Asn	His	Gln	Pro								
			280					285								

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AGGTGAAGCT	GGCCTGTTTT	CTAAAGGAAA	ATGATTGCCA	CAAGGCAAGA	GGATGCATCT	1276
TTCTTCCTGG	TGTACAAGCC	TTTAAAGACT	TCTGCTGCTG	ATATGCCTCT	TGGATGCACA	1336
CTTTGTGTGT	ACATAGTTAC	CTTTAACTCA	GTGGTTATCT	AATAGCTCTA	AACTCATTA	1396
AAAAACTCCA	AGCCTTCCAC	CAAAACAGTG	CCCCACCTGT	ATACATTTTT	ATTAAAAAAA	1456
TGTAATGCTT	ATGTATAAAC	ATGTATGTAA	TATGCTTTCT	ATGAATGATG	TTTGATTTAA	1516
ATATAATACA	TATTAATAATG	TATGGGAGAA	CCAAAAA	AAAAA		1566

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

Met 1	Phe	Asp	Lys	Thr 5	Arg	Leu	Pro	Tyr	Val 10	Ala	Leu	Asp	Val	Leu 15	Cys
Val	Leu	Leu	Ala 20	Ser	Met	Pro	Met	Ala 25	Val	Leu	Lys	Leu	Gly 30	Gln	Ile
Tyr	Pro	Phe 35	Gln	Arg	Gly	Phe	Phe 40	Cys	Lys	Asp	Asn 45	Ser	Ile	Asn	Tyr
Pro	Tyr 50	His	Asp	Ser	Thr	Ala 55	Ala	Ser	Thr	Val	Leu 60	Ile	Leu	Val	Gly
Val 65	Gly	Leu	Pro	Val	Ser 70	Ser	Ile	Ile	Leu	Gly 75	Glu	Thr	Leu	Ser	Val 80
Tyr	Cys	Asn	Leu	Leu 85	His	Ser	Asn	Ser	Phe 90	Ile	Ser	Asn	Asn	Tyr 95	Ile
Ala	Thr	Ile	Tyr 100	Lys	Ala	Ile	Gly	Thr 105	Phe	Leu	Phe	Gly	Ala 110	Ala	Ala
Ser	Gln	Ser 115	Leu	Thr	Asp	Ile	Ala 120	Lys	Tyr	Ser	Ile	Gly 125	Arg	Leu	Arg
Pro	His 130	Phe	Leu	Asp	Val	Cys 135	Asp	Pro	Asp	Trp	Ser 140	Lys	Ile	Asn	Cys
Ser 145	Asp	Gly	Tyr	Ile	Glu 150	Tyr	Tyr	Ile	Cys	Arg 155	Gly	Asn	Ala	Glu	Arg 160
Val	Lys	Glu	Gly	Arg 165	Leu	Ser	Phe	Tyr	Ser 170	Gly	His	Ser	Ser	Phe 175	Ser
Met	Tyr	Cys	Met 180	Leu	Phe	Val	Ala	Leu 185	Tyr	Leu	Gln	Ala	Arg 190	Met	Lys
Gly	Asp	Trp 195	Ala	Arg	Leu	Leu	Arg 200	Pro	Thr	Leu	Gln	Phe 205	Gly	Leu	Val
Ala	Val 210	Ser	Ile	Tyr	Val	Gly 215	Leu	Ser	Arg	Val	Ser 220	Asp	Tyr	Lys	His

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-X-

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His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala
225                      230                      235                      240

Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser
                      245                      250                      255

Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr
                      260                      265                      270

Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro
275                      280                      285

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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1362 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 294..1226

- (ix) FEATURE:
- (A) NAME/KEY: mat\_peptide
  - (B) LOCATION: 294..1226

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GGCGCAGCTC TGCAAAAGTT TCTGCTCGGG ATCTGGCTCT CTTCCCCTTG GACTTTAGAA      60
CGATTTAGGG TTAGACAGAGG AAAGCAGAGG CGCGCAGGAG GAGCAGAAAA CACCACCTTC      120
TGCAGTTGGA GGCAGGCAGC CCCGGCTGCA CTCTAGCCGC CGCGCCCGGA GCCGGGGCCG      180
ACCCGCCACT ATCCGCAGCA GCCTCGGCCA GGAGGCGACC CGGGCGCCTG GGTGTGTGGC      240
TGCTGTTGCG GGACGTCTTC GCGGGGCGGG AGGCTCGCGC CGCAGCCAGC GCC ATG      296
                                     Met
                                     1

CAA AAC TAC AAG TAC GAC AAA GCG ATC GTC CCG GAG AGC AAG AAC GGC      344
Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn Gly
5                      10                      15

GGC AGC CCG GCG CTC AAC AAC AAC CCG AGG AGG AGC GGC AGC AAG CGG      392
Gly Ser Pro Ala Leu Asn Asn Asn Pro Arg Arg Ser Gly Ser Lys Arg
20                      25                      30

GTG CTG CTC ATC TGC CTC GAC CTC TTC TGC CTC TTC ATG GCG GGC CTC      440
Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly Leu
35                      40                      45

CCC TTC CTC ATC ATC GAG ACA AGC ACC ATC AAG CCT TAC CAC CGA GGG      488
Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg Gly
50                      55                      60                      65

TTT TAC TGC AAT GAT GAG AGC ATC AAG TAC CCA CTG AAA ACT GGT GAG      536
Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly Glu
70                      75                      80

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**SECRET**



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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn  
1 5 10 15  
Gly Gly Ser Pro Ala Leu Asn Asn Asn Pro Arg Arg Ser Gly Ser Lys  
20 25 30  
Arg Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly  
35 40 45  
Leu Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg  
50 55 60  
Gly Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly  
65 70 75 80  
Glu Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly Ile Val Ile Ala  
85 90 95  
Ile Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg Ile Tyr Tyr Leu Lys  
100 105 110  
Lys Ser Arg Ser Thr Ile Gln Asn Pro Tyr Val Ala Ala Leu Tyr Lys  
115 120 125  
Gln Val Gly Cys Phe Leu Phe Gly Cys Ala Ile Ser Gln Ser Phe Thr  
130 135 140  
Asp Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu Ser  
145 150 155 160  
Val Cys Asn Pro Asp Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile  
165 170 175  
Gln Asn Tyr Arg Cys Arg Gly Asp Asp Ser Lys Val Gln Glu Ala Arg  
180 185 190  
Lys Ser Phe Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu  
195 200 205  
Tyr Leu Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg  
210 215 220  
Leu Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr  
225 230 235 240  
Thr Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val  
245 250 255  
Leu Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe  
260 265 270  
Phe Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro Ala  
275 280 285  
Pro Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile Asp Arg  
290 295 300

9

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-10-

Asn Asn His His Asn Met Met  
305 310

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..833

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 4..833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACC ATG CAG CGG AGG TGG GTC TTC GTG CTG CTC GAC GTG CTG TGC TTA 48  
Met Gln Arg Arg Trp Val Phe Val Leu Leu Asp Val Leu Cys Leu  
1 5 10 15

CTG GTC GCC TCC CTG CCC TTC GCT ATC CTG ACG CTG GTG AAC GCC CCG 96  
Leu Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn Ala Pro  
20 25 30

TAC AAG CGA GGA TTT TAC TGC GGG GAT GAC TCC ATC CGG TAC CCC TAC 144  
Tyr Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr  
35 40 45

CGT CCA GAT ACC ATC ACC CAC GGG CTC ATG GCT GGG GTC ACC ATC ACG 192  
Arg Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly Val Thr Ile Thr  
50 55 60

GCC ACC GTC ATC CTT GTC TCG GCC GGG GAA GCC TAC CTG GTG TAC ACA 240  
Ala Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr  
65 70 75

GAC CGG CTC TAT TCT CGC TCG GAC TTC AAC AAC TAC GTG GCT GCT GTA 288  
Asp Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val  
80 85 90 95

TAC AAG GTG CTG GGG ACC TTC CTG TTT GGG GCT GCC GTG AGC CAG TCT 336  
Tyr Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser  
100 105 110

CTG ACA GAC CTG GCC AAG TAC ATG ATT GGG CGT CTG AAG CCC AAC TTC 384  
Leu Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe  
115 120 125

CTA GCC GTC TGC GAC CCC GAC TGG AGC CGG GTC AAC TGC TCG GTC TAT 432  
Leu Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr  
130 135 140

GTG CAG CTG GAG AAG GTG TGC AGG GGA AAC CCT GCT GAT GTC ACC GAG 480  
Val Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu  
145 150 155

GCC AGG TTG TCT TTC TAC TCG GGA CAC TCT TCC TTT GGG ATG TAC TGC 528  
Ala Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys  
160 165 170 175

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33  
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ATG GTG TTC TTG GCG CTG TAT GTG CAG GCA CGA CTC TGT TGG AAG TGG	576
Met Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp	
180 185 190	
GCA CGG CTG CTG CGA CCC ACA GTC CAG TTC TTC CTG GTG GCC TTT GCC	624
Ala Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala	
195 200 205	
CTC TAC GTG GGC TAC ACC CGC GTG TCT GAT TAC AAA CAC CAC TGG AGC	672
Leu Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser	
210 215 220	
GAT GTC CTT GTT GGC CTC CTG CAG GGG GCA CTG GTG GCT GCC CTC ACT	720
Asp Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr	
225 230 235	
GTC TGC TAC ATC TCA GAC TTC TTC AAA GCC CGA CCC CCA CAG CAC TGT	768
Val Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys	
240 245 250 255	
CTG AAG GAG GAG GAG CTG GAA CGG AAG CCC AGC CTG TCA CTG ACG TTG	816
Leu Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu	
260 265 270	
ACC CTG GGG CGA GGC TG ACCACAACCA CTTATGGGAT ACCCGCACTC	863
Thr Leu Gly Arg Gly	
275	
TTCTTCCTGA GGCCGGACCC CGCCCAGGCA GGGAGCTGCT GTGAGTCCAG CTGATGCCCCA	923
CCCAGGTGGT CCCTCCAGCC TGGTTAGGCA CTGAGGGTTC TGGACGGGCT CCAGGAACCC	983
TGGGCTGATG GGAGCAGTGA GCGGTTCCGC TGCCCCCTGC CCTGCACTGG ACCAGGAGTC	1043
TGGAGATGCC TGGGTAGCCC TCAGCATTTG GAGGGGAACC TGTTCCCGTC GGTCCCCAAA	1103
TATCCCCTTC TTTTATGGG GTTAAGGAAG GGACCGAGAG ATCAGATAGT TGCTGTTTTG	1163
TAAAATGTAA TGTATATGTG GTTTTATAGTA AAATAGGGCA CCTGTTTCAC AAAAAAAAAA	1223
AAAAAAAAA	1232

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Gln	Arg	Arg	Trp	Val	Phe	Val	Leu	Leu	Asp	Val	Leu	Cys	Leu	Leu
1				5					10					15	
Val	Ala	Ser	Leu	Pro	Phe	Ala	Ile	Leu	Thr	Leu	Val	Asn	Ala	Pro	Tyr
			20					25					30		
Lys	Arg	Gly	Phe	Tyr	Cys	Gly	Asp	Asp	Ser	Ile	Arg	Tyr	Pro	Tyr	Arg
		35					40					45			
Pro	Asp	Thr	Ile	Thr	His	Gly	Leu	Met	Ala	Gly	Val	Thr	Ile	Thr	Ala
	50					55					60				

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Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr Asp  
 65 70 75 80  
 Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val Tyr  
 85 90 95  
 Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser Leu  
 100 105 110  
 Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe Leu  
 115 120 125  
 Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr Val  
 130 135 140  
 Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala  
 145 150 155 160  
 Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met  
 165 170 175  
 Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala  
 180 185 190  
 Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu  
 195 200 205  
 Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser Asp  
 210 215 220  
 Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr Val  
 225 230 235 240  
 Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys Leu  
 245 250 255  
 Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu Thr  
 260 265 270  
 Leu Gly Arg Gly  
 275

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Ile Cys  
 1 5 10 15  
 Val Leu Leu Ala Gly Leu Pro Phe Ala Ile Leu Thr Ser Arg His Thr  
 20 25 30  
 Pro Phe Gln Arg Gly Ile Phe Cys Asn Asp Asp Ser Ile Lys Tyr Pro  
 35 40 45  
 Tyr Lys Glu Asp Thr Ile Pro Tyr Ala Leu Leu Gly Gly Ile Val Ile  
 50 55 60

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Pro	Phe	Cys	Ile	Ile	Val	Met	Ser	Ile	Gly	Glu	Ser	Leu	Ser	Val	Tyr
65					70					75					80
Phe	Asn	Val	Leu	His	Ser	Asn	Ser	Phe	Val	Gly	Asn	Pro	Tyr	Ile	Ala
				85					90					95	
Thr	Ile	Tyr	Lys	Ala	Val	Gly	Ala	Phe	Leu	Phe	Gly	Val	Ser	Ala	Ser
			100					105					110		
Gln	Ser	Leu	Thr	Asp	Ile	Ala	Lys	Tyr	Thr	Ile	Gly	Ser	Leu	Arg	Pro
		115					120					125			
His	Phe	Leu	Ala	Ile	Cys	Asn	Pro	Asp	Trp	Ser	Lys	Ile	Asn	Cys	Ser
	130					135					140				
Asp	Gly	Tyr	Ile	Glu	Asp	Tyr	Ile	Cys	Gln	Gly	Asn	Glu	Glu	Lys	Val
145					150					155					160
Lys	Glu	Gly	Arg	Leu	Ser	Phe	Tyr	Ser	Gly	His	Ser	Ser	Phe	Ser	Met
				165					170					175	
Tyr	Cys	Met	Leu	Phe	Val	Ala	Leu	Tyr	Leu	Gln	Ala	Arg	Met	Lys	Gly
			180					185					190		
Asp	Trp	Ala	Arg	Leu	Leu	Arg	Pro	Met	Leu	Gln	Phe	Gly	Leu	Ile	Ala
		195					200					205			
Phe	Ser	Ile	Tyr	Val	Gly	Leu	Ser	Arg	Val	Ser	Asp	Tyr	Lys	His	His
	210					215					220				
Trp	Ser	Asp	Val	Thr	Val	Gly	Leu	Ile	Gln	Gly	Ala	Ala	Met	Ala	Ile
225					230					235					240
Leu	Val	Ala	Leu	Tyr	Val	Ser	Asp	Phe	Phe	Lys	Asp	Thr	His	Ser	Tyr
				245					250					255	
Lys	Glu	Arg	Lys	Glu	Glu	Asp	Pro	His	Thr	Thr	Leu	His	Glu	Thr	Ala
			260					265					270		
Ser	Ser	Arg	Asn	Tyr	Ser	Thr	Asn	His	Glu	Pro					
			275				280								

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Phe	Asp	Lys	Thr	Arg	Leu	Pro	Tyr	Val	Ala	Leu	Asp	Val	Leu	Cys
1				5					10					15	
Val	Leu	Leu	Ala	Gly	Leu	Pro	Phe	Ala	Ile	Leu	Thr	Ser	Arg	His	Thr
			20					25					30		
Pro	Phe	Gln	Arg	Gly	Val	Phe	Cys	Asn	Asp	Glu	Ser	Ile	Lys	Tyr	Pro
		35					40					45			
Tyr	Lys	Glu	Asp	Thr	Ile	Pro	Tyr	Ala	Leu	Leu	Gly	Gly	Ile	Ile	Ile
	50					55					60				

Pro Phe Ser Ile Ile Val Ile Ile Leu Gly Glu Thr Leu Ser Val Tyr  
65 70 75 80

Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile Ala  
85 90 95

Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala Ser  
100 105 110

Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg Pro  
115 120 125

His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys Ser  
130 135 140

Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg Val  
145 150 155 160

Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser Met  
165 170 175

Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys Gly  
180 185 190

Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val Ala  
195 200 205

Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His His  
210 215 220

Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala Ile  
225 230 235 240

Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser Phe  
245 250 255

Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr Pro  
260 265 270

Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro  
275 280

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 285 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Phe Asp Lys Thr Arg Leu Pro Tyr Val Ala Leu Asp Val Leu Cys  
1 5 10 15

Val Leu Leu Ala Ser Met Pro Met Ala Val Leu Lys Leu Gly Gln Ile  
20 25 30

Tyr Pro Phe Gln Arg Gly Phe Phe Cys Lys Asp Asn Ser Ile Asn Tyr  
35 40 45

Pro Tyr His Asp Ser Thr Ala Ala Ser Thr Val Leu Ile Leu Val Gly  
50 55 60

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Val Gly Leu Pro Val Ser Ser Ile Ile Leu Gly Glu Thr Leu Ser Val  
65 70 75 80

Tyr Cys Asn Leu Leu His Ser Asn Ser Phe Ile Arg Asn Asn Tyr Ile  
85 90 95

Ala Thr Ile Tyr Lys Ala Ile Gly Thr Phe Leu Phe Gly Ala Ala Ala  
100 105 110

Ser Gln Ser Leu Thr Asp Ile Ala Lys Tyr Ser Ile Gly Arg Leu Arg  
115 120 125

Pro His Phe Leu Asp Val Cys Asp Pro Asp Trp Ser Lys Ile Asn Cys  
130 135 140

Ser Asp Gly Tyr Ile Glu Tyr Tyr Ile Cys Arg Gly Asn Ala Glu Arg  
145 150 155 160

Val Lys Glu Gly Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Ser  
165 170 175

Met Tyr Cys Met Leu Phe Val Ala Leu Tyr Leu Gln Ala Arg Met Lys  
180 185 190

Gly Asp Trp Ala Arg Leu Leu Arg Pro Thr Leu Gln Phe Gly Leu Val  
195 200 205

Ala Val Ser Ile Tyr Val Gly Leu Ser Arg Val Ser Asp Tyr Lys His  
210 215 220

His Trp Ser Asp Val Leu Thr Gly Leu Ile Gln Gly Ala Leu Val Ala  
225 230 235 240

Ile Leu Val Ala Val Tyr Val Ser Asp Phe Phe Lys Glu Arg Thr Ser  
245 250 255

Phe Lys Glu Arg Lys Glu Glu Asp Ser His Thr Thr Leu His Glu Thr  
260 265 270

Pro Thr Thr Gly Asn His Tyr Pro Ser Asn His Gln Pro  
275 280 285

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gln Asn Tyr Lys Tyr Asp Lys Ala Ile Val Pro Glu Ser Lys Asn  
1 5 10 15

Gly Gly Ser Pro Ala Leu Asn Asn Asn Pro Arg Arg Ser Gly Ser Lys  
20 25 30

Arg Val Leu Leu Ile Cys Leu Asp Leu Phe Cys Leu Phe Met Ala Gly  
35 40 45

Leu Pro Phe Leu Ile Ile Glu Thr Ser Thr Ile Lys Pro Tyr His Arg  
50 55 60

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Gly Phe Tyr Cys Asn Asp Glu Ser Ile Lys Tyr Pro Leu Lys Thr Gly  
 65 70 75 80  
 Glu Thr Ile Asn Asp Ala Val Leu Cys Ala Val Gly Ile Val Ile Ala  
 85 90 95  
 Ile Leu Ala Ile Ile Thr Gly Glu Phe Tyr Arg Ile Tyr Tyr Leu Lys  
 100 105 110  
 Lys Ser Arg Ser Thr Ile Gln Asn Pro Tyr Val Ala Ala Leu Tyr Lys  
 115 120 125  
 Gln Val Gly Cys Phe Leu Phe Gly Cys Ala Ile Ser Gln Ser Phe Thr  
 130 135 140  
 Asp Ile Ala Lys Val Ser Ile Gly Arg Leu Arg Pro His Phe Leu Ser  
 145 150 155 160  
 Val Cys Asn Pro Asp Phe Ser Gln Ile Asn Cys Ser Glu Gly Tyr Ile  
 165 170 175  
 Gln Asn Tyr Arg Cys Arg Gly Asp Asp Ser Lys Val Gln Glu Ala Arg  
 180 185 190  
 Lys Ser Phe Phe Ser Gly His Ala Ser Phe Ser Met Tyr Thr Met Leu  
 195 200 205  
 Tyr Leu Val Leu Tyr Leu Gln Ala Arg Phe Thr Trp Arg Gly Ala Arg  
 210 215 220  
 Leu Leu Arg Pro Leu Leu Gln Phe Thr Leu Ile Met Met Ala Phe Tyr  
 225 230 235 240  
 Thr Gly Leu Ser Arg Val Ser Asp His Lys His His Pro Ser Asp Val  
 245 250 255  
 Leu Ala Gly Phe Ala Gln Gly Ala Leu Val Ala Cys Cys Ile Val Phe  
 260 265 270  
 Phe Val Ser Asp Leu Phe Lys Thr Lys Thr Thr Leu Ser Leu Pro Ala  
 275 280 285  
 Pro Ala Ile Arg Lys Glu Ile Leu Ser Pro Val Asp Ile Ile Asp Arg  
 290 295 300  
 Asn Asn His His Asn Met Met  
 305 310

## (2) INFORMATION FOR SEQ ID NO:13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Gln Arg Arg Trp Val Phe Val Leu Leu Asp Val Leu Cys Leu Leu  
 1 5 10 15  
 Val Ala Ser Leu Pro Phe Ala Ile Leu Thr Leu Val Asn Ala Pro Tyr  
 20 25 30

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Lys Arg Gly Phe Tyr Cys Gly Asp Asp Ser Ile Arg Tyr Pro Tyr Arg  
35 40 45

Pro Asp Thr Ile Thr His Gly Leu Met Ala Gly Val Thr Ile Thr Ala  
50 55 60

Thr Val Ile Leu Val Ser Ala Gly Glu Ala Tyr Leu Val Tyr Thr Asp  
65 70 75 80

Arg Leu Tyr Ser Arg Ser Asp Phe Asn Asn Tyr Val Ala Ala Val Tyr  
85 90 95

Lys Val Leu Gly Thr Phe Leu Phe Gly Ala Ala Val Ser Gln Ser Leu  
100 105 110

Thr Asp Leu Ala Lys Tyr Met Ile Gly Arg Leu Lys Pro Asn Phe Leu  
115 120 125

Ala Val Cys Asp Pro Asp Trp Ser Arg Val Asn Cys Ser Val Tyr Val  
130 135 140

Gln Leu Glu Lys Val Cys Arg Gly Asn Pro Ala Asp Val Thr Glu Ala  
145 150 155 160

Arg Leu Ser Phe Tyr Ser Gly His Ser Ser Phe Gly Met Tyr Cys Met  
165 170 175

Val Phe Leu Ala Leu Tyr Val Gln Ala Arg Leu Cys Trp Lys Trp Ala  
180 185 190

Arg Leu Leu Arg Pro Thr Val Gln Phe Phe Leu Val Ala Phe Ala Leu  
195 200 205

Tyr Val Gly Tyr Thr Arg Val Ser Asp Tyr Lys His His Trp Ser Asp  
210 215 220

Val Leu Val Gly Leu Leu Gln Gly Ala Leu Val Ala Ala Leu Thr Val  
225 230 235 240

Cys Tyr Ile Ser Asp Phe Phe Lys Ala Arg Pro Pro Gln His Cys Leu  
245 250 255

Lys Glu Glu Glu Leu Glu Arg Lys Pro Ser Leu Ser Leu Thr Leu Thr  
260 265 270

Leu Gly Arg Gly  
275

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 29 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCTCTAGAT ATTAATAGTA ATCAATTAC

29

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:

- 9
- 40  
-18-
- (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCACGCAT GCACCATGGT AATAGC

26

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTGTCATGCG TGAGGCTCCG GTGC

24

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTAAGTTTCA CGGTACCTGA AATGGAAG

28

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCATGGTAC CATGTTTGAC AAGACGCGGC

30

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CATATGTAGT ATTCAATGTA ACC

23

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 47 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TGATGGCTAG CATGCAGAGA AGATGGGTCT TCGTGCTGCT CGACGTG

47

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGTGCGGGAT CCCATAAGTG GTTG

24

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